



	34	43	39	42	48	31	25	26	28	30																																	
hApo2LI	D	C	A	G	D	-	-	F	H	K	I	G	L	F	C	C	R	G	C	P	A	G	H	Y	L	K	A	P	C	T	E	P	C	G	N	S	T	C	L				
hTNFR1	V	C	P	O	G	K	-	-	Y	I	H	P	O	N	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	N	D	C	P	G	P	G	O	D	T	D	C	R		
hTNFR2	T	C	R	L	R	E	-	-	Y	Y	D	Q	T	A	Q	M	C	C	S	K	C	S	P	G	Q	H	A	K	V	F	C	T	K	T	-	S	D	T	V	C	D		
hTNFRip	T	C	R	D	Q	E	K	E	-	Y	Y	E	P	Q	H	R	I	C	C	S	R	C	P	P	G	T	Y	V	S	A	K	C	S	R	I	-	R	D	T	V	C	A	
hFAS/Apo1	N	L	E	G	L	-	-	-	-	H	H	D	G	Q	F	C	H	K	P	C	P	P	G	E	R	K	A	R	D	C	T	V	N	G	D	E	P	D	C	V			
hLINGR	A	C	P	T	G	-	-	-	-	L	Y	T	H	S	G	E	C	K	A	C	N	L	G	E	G	V	A	Q	P	C	G	A	-	-	N	Q	T	V	C	E			
hCD40	A	C	R	E	K	-	-	-	-	Q	Y	L	I	N	S	Q	C	C	S	L	C	Q	P	G	Q	K	L	V	S	D	C	T	E	F	-	T	E	T	E	C	L		
hCD27	S	C	P	E	R	-	-	-	-	H	Y	W	A	Q	G	K	L	C	C	Q	M	C	E	P	G	T	F	L	V	K	D	C	D	Q	H	R	K	A	Q	C	D		
hCD30	T	C	H	G	N	P	S	H	-	Y	Y	D	K	A	V	R	R	C	C	Y	R	C	P	M	G	L	F	P	T	Q	Q	C	P	Q	R	-	-	P	T	D	C	R	K
hOx40	H	C	V	G	D	T	-	-	-	Y	P	S	N	D	R	C	C	H	E	C	R	P	P	G	G	N	G	M	V	S	R	C	S	R	S	-	Q	N	T	V	C	R	

hApO2LI	72	V	C	P	Q	D	-	T	F	L	A	W	E	N	H	H	S	E	C	A	R	C	-	Q	A	C	D	E	Q	A	S	Q	V	A	L	E	N	C	S	A	V	A	D	T	R	C	G
hTNFR1	83	E	C	E	S	G	-	S	F	T	A	S	E	N	H	L	R	H	C	L	S	C	-	S	K	C	R	K	E	M	Q	V	E	I	S	S	C	T	V	D	R	D	T	V	C	G	
hTNFR2	77	S	C	E	D	S	T	Y	T	Q	L	W	N	W	V	-	P	E	C	L	S	C	G	S	R	C	S	S	-	D	Q	V	E	T	Q	A	C	T	R	E	Q	N	R	I	C	T	
hTNFRtp	82	T	C	A	E	N	S	Y	N	E	H	W	N	Y	L	-	T	I	C	Q	L	C	-	R	P	C	D	P	V	M	G	L	E	E	I	A	P	C	T	S	K	R	K	T	Q	C	R
hFAS/Apo1	84	P	C	Q	E	G	K	E	Y	T	D	K	A	H	F	S	S	K	C	R	R	C	-	R	L	C	D	E	G	H	G	L	E	V	E	I	N	C	T	R	T	Q	N	T	K	C	R
hLINGFR	66	P	C	L	D	S	V	T	F	S	D	V	V	S	A	T	E	P	C	K	P	C	-	T	E	C	V	G	L	-	Q	S	M	S	A	P	C	V	E	A	D	D	A	V	C	R	
hCD40	61	P	C	G	E	S	E	F	L	D	T	W	N	R	E	-	T	H	C	H	Q	H	-	K	Y	C	D	P	N	L	G	L	R	V	Q	Q	K	G	T	S	E	T	D	T	I	C	T
hCD27	64	P	C	I	P	G	V	S	F	S	P	D	H	H	T	R	P	H	C	E	S	C	-	R	H	C	N	S	G	L	L	V	R	-	-	N	C	T	I	T	A	N	A	E	C	A	
hCD30	68	Q	C	E	P	D	-	Y	Y	L	D	E	A	D	R	-	-	-	C	T	A	C	-	V	T	C	S	R	D	D	L	V	E	K	T	-	P	C	A	W	N	S	S	R	V	C	E
hOX40	66	P	C	G	P	G	-	F	Y	N	D	V	V	S	S	K	P	-	C	K	P	C	-	T	W	C	N	L	R	S	G	S	E	R	K	Q	L	C	T	A	T	Q	D	T	V	C	R

**FIG. 2A**

hApo2LI	116	CCKPGWFVECVSQCVSSSPFYCQPCLDCCGALHRRTRLCSRRD-TDCG-T
htNFR1	127	CRKNQYRHYWSENL--FQCFCNCSLCLNG--TVHLSCQEKNNTVC--T
htNFR2	120	CRPGWYCALSKEGC---RLCAPLRKCRPG-FGVARPGETETSDVVCK-P
htNFRip	126	CQPGMFCAAWALEC---THCELLSDCPPGTAEELKDEVGKGNNHCVP-P
hFAS/Apol	129	CKPNFF-CNSTVC---EHCDPCTKCEHGI---IKECTLTSNTKCK-
hLNGFR	109	CAYGY YQDETT---GRCEACRVCEAGSGL-VFSCQDKQNNTVCE-E
hCD40	105	CEEGW HCTSEAC---ESCVLHRS CSPGGF-VKQIATGVSDTI CE-P
hCD27	106	CRNGWQCRDKEC---TECDPLPNPSLTARSSQALSHPQPPTHLP-
hCD30	108	- CRPGMFCSTSAVN SC - - ARCFFHSVCPAGMIVKFPGTAQK-NTVCE-
hOX40	109	- CRA GTQPLDSYKPG - - - VDCA - - - - - - - - - - - - -

**FIG. 2B**

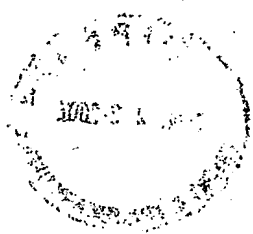
1081 GGGCCCGCAG CTCTACGACG TGATGGACGC GGTCCACGCG CGGCGCTGGA AGGAGTTTCGT  
 332 G P Q L Y D V M D A V P A R R W K E F V  
  
 1141 GCGCAGCGTG GGGCTGCGCG AGGCAGAGAT CGAAGCCGTG GAGGTGGAGA TCGGCCGCTT  
 352 R T L G L R E A E I E A V E V E I G R F  
  
 1201 CCGAGACCAG CAGTACGAGA TGCTCAAGCG CTGGCGCCAG CAGCAGCCCG CGGGCCTCGG  
 372 R D Q Q Y E M L K R W R Q Q Q P A G L G  
  
 1261 AGCCGTTTAC GCGGCCCTGG AGCGCATGGG GCTGGACGGC TGGGTGGAG ACTTGCGCAG  
 392 A V Y A A L E R M G L D G C V E D L R S  
  
 1321 CCGCCTGCAG CGCGGCCCGT GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC  
 412 R L Q R G P  
  
 1381 TTGCAGAAGC CCTAAGTACG GTTACTATG CGGTAGACA TTTTATGTCA CTTATTAAGC  
  
 1441 CGCTGGCAGC GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC CCCTATCGCT  
  
 1501 CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG GTGAAGACAT TTCTCAACTT  
  
 1561 CTCGGCCGGA GTTTGGCTGA GATCGCGGTA TTAAATCTGT GAAAGAAAC AAAAAAAAAA  
  
 1621 AAAAAAAAAA AAAA

FIG. 4C



1 CGGGCCCTGC GGGCGCGGG CTGAAGCGG AACACGAGC GGCAGAGAGC ACGAGCCGG  
 61 GAAGCCCTG GGCGCCCGTC GGAGGGCTAT GGAGCAGCGG CCGCGGGGCT GCGCGGGGT  
 1 M E O R P R G C A A V  
 121 GCGCGCGCG CTCCTCCTGG TGCTGCTGG GGC CGCGGGCA CTCGTAGCCC  
 12 A A A L L L V L L G A R A Q G G T R S P  
 181 CAGGTGTGAC TGTGCCGGTG ACTTCCACAA GAAGATTGGT CTGTTTGTG GCAGAGGCTG  
 32 R C D C A G D F H K K I G L F C C R G C  
 241 CCCAGCGGG CACTACCTGA AGGCCCTTG CACGGAGCCC TCGGGCAACT CCACCTGCCT  
 52 P A G H Y L K A P C T E P C G N S T C L  
 301 TGTGTGTCCC CAAGACACCT TCTTGGCCTG GGAGAACCAC CATAATTCTG AATGTGCCCC  
 72 V C P Q D T F L A W E N H H N S E C A R  
 361 CTGCCAGGCC TGTGATGAGC AGGCTTCCCA GGTGGCGCTG GAGAACTGTT CAGCAGTGGC  
 92 C Q A C D E Q A S Q V A L E N C S A V A  
 421 CGACACCCGC TGTGGCTGTA AGCCAGGCTG GTTGTGGAG TCCAGGTCA GCCAATGTGT  
 112 D T R C G C K P G W F V E C Q V S Q C V  
 481 CAGCAGTTCA CCCTTCTACT GCCAACCATG CCTAGACTGC GGGGCCCTGC ACCGCCACAC  
 132 S S S P F Y C Q P C L D C G A L H R H T

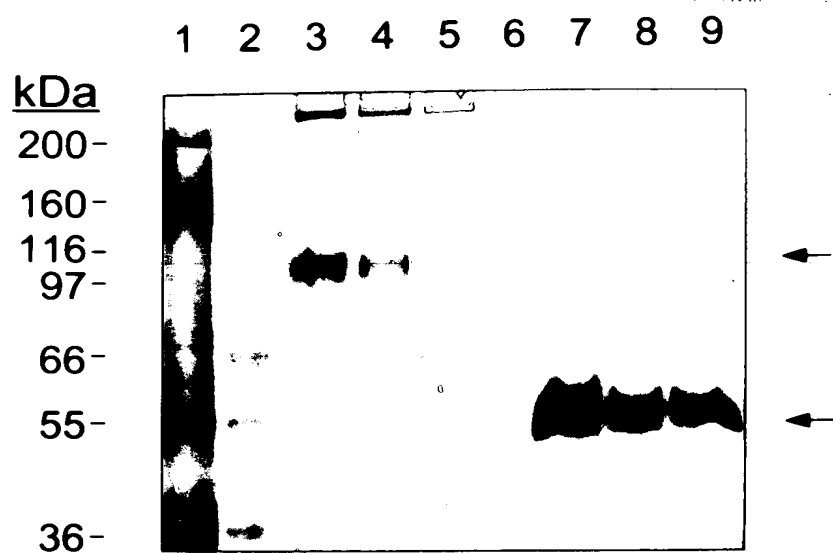
FIG. 4A











**FIG. 3**

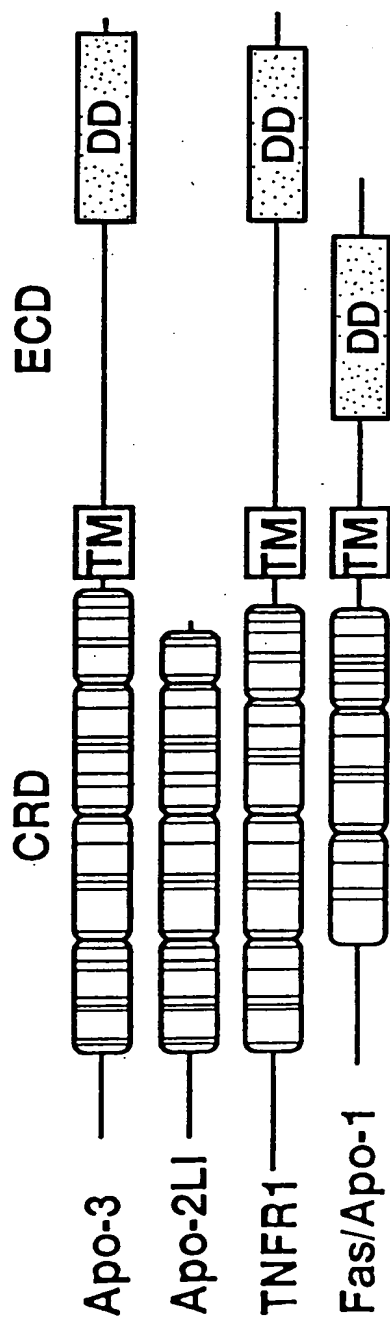
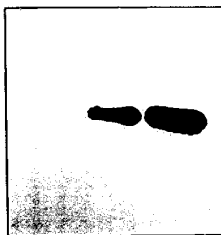


FIG. 7



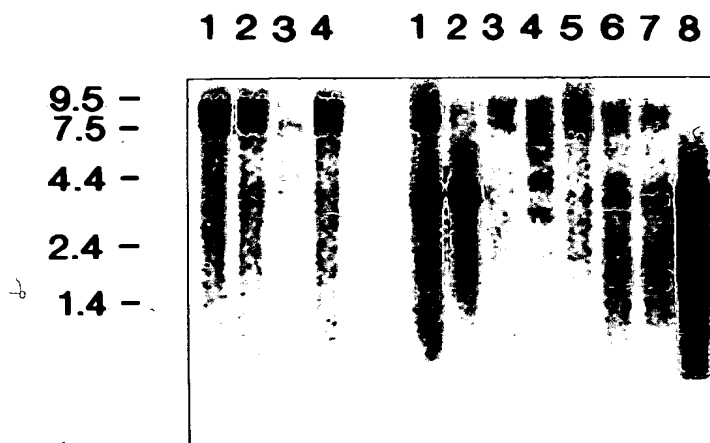
**Transfection**

**pRK5**  
**TNFR1**  
**Apo-3**



◀ **Phospho-C-Jun**

**FIG. 11**



**FIG. 12**

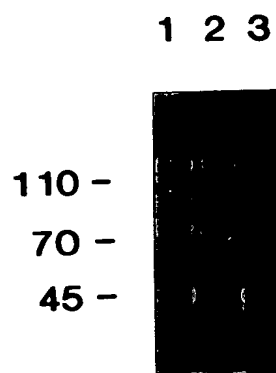
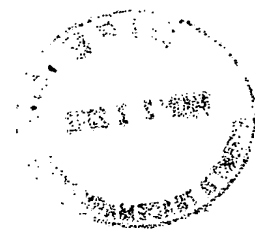


FIG. 8

1 2 3 4 5 6 7 8 9

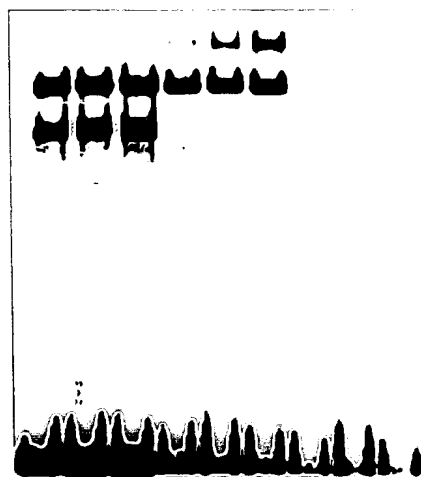


FIG. 10

FIG. 9A

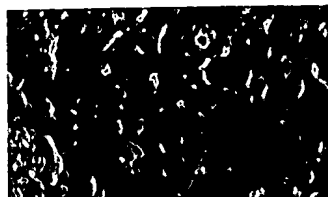


FIG. 9B



FIG. 9C



FIG. 9D

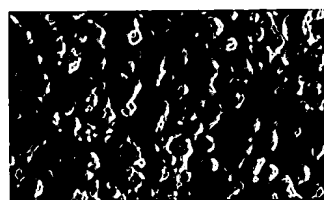


FIG. 9E

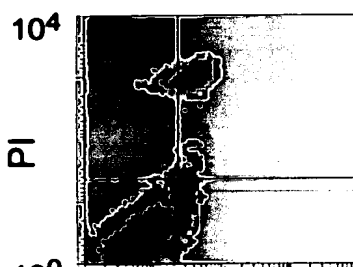


FIG. 9F

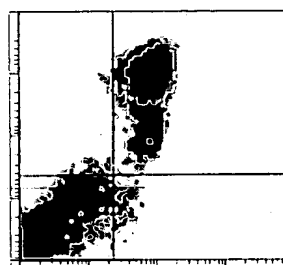


FIG. 9G

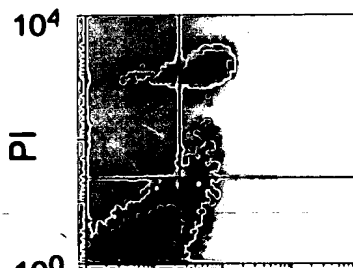
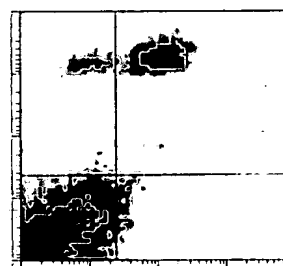


FIG. 9H



Annexin-V-FITC

FIG. 9I

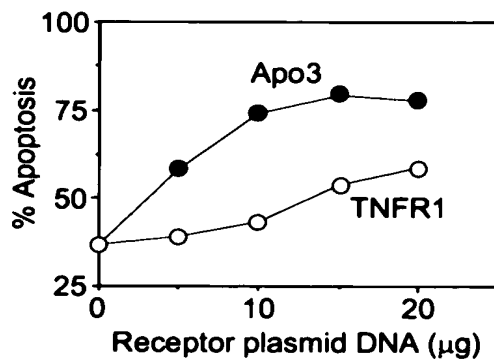


FIG. 9J